

MAR 25 2002

LeA34821\_SeqList

SEQUENCE LISTING

<110> Bayer Aktiengesellschaft

<120> Acetylcholine receptor subunits

<130> Le A 34 821

<140> US/09/941,179

<141> 2001-08-27

<150> DE 100 42 177.6

<151> 2000-08-28

<160> 17

<170> PatentIn Ver. 2.1

<210> 1

<211> 45

<212> PRT

<213> Torpedo californica

<400> 1

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Lys Ile Met Trp Thr Pro Pro Ala Ile Phe Lys Ser Tyr Cys Glu Ile  
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Ile Val Thr His Phe Pro Phe Asp Gln Gln Asn Cys Thr  
35 40 45

<210> 2

<211> 1869

<212> DNA

<213> Artificial sequence

<220>

<221> CDS

<222> (1)..(1866)

<223> Description of Artificial Sequence: Modified alpha  
4 subunit of the chicken nicotinic acetylcholine  
receptor

<400> 2

atg gga ttt ctc gtg tcg aag gga aac ctc ctc ctc ctg ctg tgt gcc  
Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Cys Ala  
1 5 10 15 48

agc atc ttc ccc gct ttc ggc cac gtg gaa acg cga gcc cat gcg gag  
Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu  
20 25 30 96

gag cgc ctc ctg aag aaa ctc ttc tcc ggg tat aac aag tgg tcc cgt  
Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg  
35 40 45 144

ccc gtc gcc aac att tcg gat gtg gtc ctg gtc cgc ttc ggc ttg tcc  
Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser  
50 55 60 192

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ata gcc cag ctc atc gat gtt gat gag aag aac caa atg atg acc aca Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr 65 70 75 80	240
aat gtg tgg gtg aag cag gag tgg cac gac tac aag ctg cgc tgg gac Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp 85 90 95	288
ccc cag gag tat gaa aac gtc aca tcc atc cga atc ccc tca gag ctc Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu 100 105 110	336
atc tgg cgg ccg gac ata gtc ctc tac aac aat gcc gac ggc aac ttc Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asn Phe 115 120 125	384
gag gta acg ctg gcg acg aag gcg act ttg aat tat acg gga cgt gtg Glu Val Thr Leu Ala Thr Lys Ala Thr Leu Asn Tyr Thr Gly Arg Val 130 135 140	432
gag tgg cgc ccg ccg gct atc tac aag tcc tcg tgc gag atc gac gtg Glu Trp Arg Pro Pro Ala Ile Tyr Lys Ser Ser Cys Glu Ile Asp Val 145 150 155 160	480
gaa tac ttc ccg ttc gac cag cag acg tgc gtc atg aag ttc ggc tcg Glu Tyr Phe Pro Phe Asp Gln Gln Thr Cys Val Met Lys Phe Gly Ser 165 170 175	528
tgg aca tat gac aaa gct aag ata gac ttg gtg agc atg cat agc cat Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His 180 185 190	576
gtg gac caa ctg gac tac tgg gaa agc ggg gag tgg gtc atc att aat Val Asp Gln Leu Asp Tyr Trp Glu Ser Gly Glu Trp Val Ile Ile Asn 195 200 205	624
gcc gtg ggc aat tac aac agc aag aaa tat gaa tgc tgc aca gag atc Ala Val Gly Asn Tyr Asn Ser Lys Lys Tyr Glu Cys Cys Thr Glu Ile 210 215 220	672
tac cct gat ata act tac tcc ttc att atc cgg agg ctg ccg ctg ttc Tyr Pro Asp Ile Thr Tyr Ser Phe Ile Ile Arg Arg Leu Pro Leu Phe 225 230 235 240	720
tac aca atc aat ttg atc att ccc tgc ctg ctt atc tcc tgc ttg act Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile Ser Cys Leu Thr 245 250 255	768
gtc ctg gtc ttc tac cta ccc tct gag tgc gga gag aag ata acc ttg Val Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly Glu Lys Ile Thr Leu 260 265 270	816
tgc atc tct gtg ctg cta tcc ctc acg gtg ttc ctg ctg ctc atc aca Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu Ile Thr 275 280 285	864
gag atc atc cct tct acc tcc ctg gtc atc ccc ctg ata gga gag tat Glu Ile Ile Pro Ser Thr Ser Leu Val Ile Pro Leu Ile Gly Glu Tyr 290 295 300	912
ctg ctc ttc acc atg ata ttt gtc acc ttg tct atc atc atc act gtc Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Ile Ile Thr Val 305 310 315 320	960

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Asp Trp Val Arg Arg Val Phe Leu Asp Ile Val Pro Arg Leu Leu Phe	
340 345 350	
atg aag cgg ccc tcc aca gtg aaa gac aat tgc aag aag ctt att gaa	1104
Met Lys Arg Pro Ser Thr Val Lys Asp Asn Cys Lys Lys Leu Ile Glu	
355 360 365	
tct atg cac aaa cta acc aac tca cca agg ctt tgg tct gag acc gac	1152
Ser Met His Lys Leu Thr Asn Ser Pro Arg Leu Trp Ser Glu Thr Asp	
370 375 380	
atg gag ccc aac ttc act acc tca tcc tcc ccc agc ccc cag agt aat	1200
Met Glu Pro Asn Phe Thr Thr Ser Ser Ser Pro Ser Pro Gln Ser Asn	
385 390 395 400	
gaa cct tca ccc aca tct tcc ttc tgt gcc cac ctt gag gag cca gcc	1248
Glu Pro Ser Pro Thr Ser Ser Phe Cys Ala His Leu Glu Glu Pro Ala	
405 410 415	
aaa cct atg tgc aaa tcc cct tct gga cag tac tca atg ctg cac cct	1296
Lys Pro Met Cys Lys Ser Pro Ser Gly Gln Tyr Ser Met Leu His Pro	
420 425 430	
gag ccc cca cag gtg acg tgt tcc tct ccg aag ccc tcc tgc cac ccc	1344
Glu Pro Pro Gln Val Thr Cys Ser Ser Pro Lys Pro Ser Cys His Pro	
435 440 445	
ctg agt gac acc cag acc aca tct atc tca aaa ggc aga tcg ctc agt	1392
Leu Ser Asp Thr Gln Thr Thr Ser Ile Ser Lys Gly Arg Ser Leu Ser	
450 455 460	
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Val Gln Gln Met Tyr Ser Pro Asn Lys Thr Glu Glu Gly Ser Ile Arg	
465 470 475 480	
tgt agg tcc cga agc atc cag tac tgt tac ctg cag gag gac tct tcc	1488
Cys Arg Ser Arg Ser Ile Gln Tyr Cys Tyr Leu Gln Glu Asp Ser Ser	
485 490 495	
cag acc aat ggc cac tct agt gcc tct cca gcg tcg cag cgc tgc cac	1536
Gln Thr Asn Gly His Ser Ser Ala Ser Pro Ala Ser Gln Arg Cys His	
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ctc aat gaa gag cag ccc cag cac aag ccc cac cag tgc aag tgt aag	1584
Leu Asn Glu Gln Pro Gln His Lys Pro His Gln Cys Lys Cys Lys	
515 520 525	
tgc aga aag gga gag gca gct ggc aca ccg act caa gga agc aag agc	1632
Cys Arg Lys Gly Glu Ala Ala Gly Thr Pro Thr Gln Gly Ser Lys Ser	
530 535 540	
cac agc aac aaa gga gaa cac ctc gtg ctg atg tcc cca gcc ctg aag	1680
His Ser Asn Lys Gly Glu His Leu Val Leu Met Ser Pro Ala Leu Lys	
545 550 555 560	
ctg gcg gtg gaa ggg gtc cac tac att gca gac cac ctg cga gca gaa	1728
Leu Ala Val Glu Gly Val His Tyr Ile Ala Asp His Leu Arg Ala Glu	

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575

gat gca gat ttc tca gtg aag gaa gac tgg aag tac gta gca atg gtc 1776  
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 580 585 590

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 Ile Asp Arg Ile Phe Leu Trp Met Phe Ile Ile Val Cys Leu Leu Gly  
 595 600 605

acc gtt ggg ctc ttc ctc ccg ccg tgg ctg gca gga atg atc taa 1869  
 Thr Val Gly Leu Phe Leu Pro Pro Trp Leu Ala Gly Met Ile  
 610 615 620

&lt;210&gt; 3

&lt;211&gt; 622

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Modified alpha  
 4 subunit of the chicken nicotinic acetylcholine  
 receptor

&lt;400&gt; 3

Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Cys Ala  
 1 5 10 15

Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu  
 20 25 30

Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg  
 35 40 45

Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser  
 50 55 60

Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr  
 65 70 75 80

Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp  
 85 90 95

Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu  
 100 105 110

Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asn Phe  
 115 120 125

Glu Val Thr Leu Ala Thr Lys Ala Thr Leu Asn Tyr Thr Gly Arg Val  
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Glu Trp Arg Pro Pro Ala Ile Tyr Lys Ser Ser Cys Glu Ile Asp Val  
 145 150 155 160

Glu Tyr Phe Pro Phe Asp Gln Gln Thr Cys Val Met Lys Phe Gly Ser  
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Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His  
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Val Asp Gln Leu Asp Tyr Trp Glu Ser Gly Glu Trp Val Ile Ile Asn

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Ala Val Gly Asn Tyr Asn Ser Lys Lys Tyr Glu Cys Cys Thr Glu Ile		
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Tyr Pro Asp Ile Thr Tyr Ser Phe Ile Ile Arg Arg Leu Pro Leu Phe		
225	230	235
240		
Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile Ser Cys Leu Thr		
245	250	255
Val Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly Glu Lys Ile Thr Leu		
260	265	270
Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu Leu Ile Thr		
275	280	285
Glu Ile Ile Pro Ser Thr Ser Leu Val Ile Pro Leu Ile Gly Glu Tyr		
290	295	300
Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Ile Ile Thr Val		
305	310	315
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325	330	335
Asp Trp Val Arg Arg Val Phe Leu Asp Ile Val Pro Arg Leu Leu Phe		
340	345	350
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355	360	365
Ser Met His Lys Leu Thr Asn Ser Pro Arg Leu Trp Ser Glu Thr Asp		
370	375	380
Met Glu Pro Asn Phe Thr Thr Ser Ser Pro Ser Pro Gln Ser Asn		
385	390	395
400		
Glu Pro Ser Pro Thr Ser Ser Phe Cys Ala His Leu Glu Glu Pro Ala		
405	410	415
Lys Pro Met Cys Lys Ser Pro Ser Gly Gln Tyr Ser Met Leu His Pro		
420	425	430
Glu Pro Pro Gln Val Thr Cys Ser Ser Pro Lys Pro Ser Cys His Pro		
435	440	445
Leu Ser Asp Thr Gln Thr Thr Ser Ile Ser Lys Gly Arg Ser Leu Ser		
450	455	460
Val Gln Gln Met Tyr Ser Pro Asn Lys Thr Glu Glu Gly Ser Ile Arg		
465	470	475
480		
Cys Arg Ser Arg Ser Ile Gln Tyr Cys Tyr Leu Gln Glu Asp Ser Ser		
485	490	495
Gln Thr Asn Gly His Ser Ser Ala Ser Pro Ala Ser Gln Arg Cys His		
500	505	510
Leu Asn Glu Glu Gln Pro Gln His Lys Pro His Gln Cys Lys Cys Lys		
515	520	525
Cys Arg Lys Gly Glu Ala Ala Gly Thr Pro Thr Gln Gly Ser Lys Ser		

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His Ser Asn Lys Gly Glu His Leu Val Leu Met Ser Pro Ala Leu Lys		
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Leu Ala Val Glu Gly Val His Tyr Ile Ala Asp His Leu Arg Ala Glu		
565	570	575
Asp Ala Asp Phe Ser Val Lys Glu Asp Trp Lys Tyr Val Ala Met Val		
580	585	590
Ile Asp Arg Ile Phe Leu Trp Met Phe Ile Ile Val Cys Leu Leu Gly		
595	600	605
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

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<210> 5  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 5  
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<210> 6  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)..(1893)  
 <223> Description of Artificial Sequence: Modified alpha  
 4 subunit of the chicken nicotinic acetylcholine  
 receptor

<400> 6  
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 Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Cys Ala  
 1 5 10 15

agc atc ttc ccc gct ttc ggc cac gtg gaa acg cga gcc cat gcg gag 96  
 Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu  
 20 25 30

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gag cgc ctc ctg aag aaa ctc ttc tcc ggg tat aac aag tgg tcc cgt	144
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ccc gtc gcc aac att tcg gat gtc gtc ctg gtc cgc ttc ggc ttg tcc	192
Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser	
50 55 60	
ata gcc cag ctc atc gat gtt gat gag aag aac caa atg atg acc aca	240
Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr	
65 70 75 80	
aat gtg tgg gtg aag cag gag tgg cac gac tac aag ctg cgc tgg gac	288
Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp	
85 90 95	
ccc cag gag tat gaa aac gtc aca tcc atc cga atc ccc tca gag ctc	336
Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu	
100 105 110	
atc tgg agg ccg gac att gtc cta tac aac aat gct gat ggt gac ttt	384
Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe	
115 120 125	
gca gtc acc cac ctg acc aaa gcc cac ctc ttc tat gat ggg aga att	432
Ala Val Thr His Leu Thr Lys Ala His Leu Phe Tyr Asp Gly Arg Ile	
130 135 140	
aaa tgg atg cca cct gcc atc tac aaa agc tcc tgc agc atc gat gtt	480
Lys Trp Met Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser Ile Asp Val	
145 150 155 160	
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Thr Phe Phe Pro Phe Asp Gln Gln Asn Cys Lys Met Lys Phe Gly Ser	
165 170 175	
tgg aca tat gac aaa gct aag ata gac ttg gtg agc atg cat agc cat	576
Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His	
180 185 190	
cgc ggg acc aac gtg gtg gag ctg ggc gtg gac caa ctg gac tac tgg	624
Arg Gly Thr Asn Val Val Glu Leu Gln Val Asp Gln Leu Asp Tyr Trp	
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gaa agc ggg gag tgg gtc atc att aat gcc gtg ggc aat tac aac agc	672
Glu Ser Gly Glu Trp Val Ile Ile Asn Ala Val Gly Asn Tyr Asn Ser	
210 215 220	
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Lys Lys Tyr Glu Cys Cys Thr Glu Ile Tyr Pro Asp Ile Thr Tyr Ser	
225 230 235 240	
ttc att atc cgg agg ctg ccg ctg ttc tac aca atc aat ttg atc att	768
Phe Ile Ile Arg Arg Leu Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile	
245 250 255	
ccc tgc ctg ctt atc tcc tgc ttg act gtc ctg gtc ttc tac cta ccc	816
Pro Cys Leu Leu Ile Ser Cys Leu Thr Val Leu Val Phe Tyr Leu Pro	
260 265 270	
tct gag tgc gga gag aag ata acc ttg tgc atc tct gtg ctg cta tcc	864
Ser Glu Cys Gly Glu Lys Ile Thr Leu Cys Ile Ser Val Leu Leu Ser	

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gtc acc ttg tct atc atc atc act gtc ttt gtg ctc aac gta cac cac Val Thr Leu Ser Ile Ile Thr Val Phe Val Leu Asn Val His His 325 330 335			1008
cgt tca cca cgt acc cac acg atg cct gac tgg gtg agg agg gtc ttc Arg Ser Pro Arg Thr His Thr Met Pro Asp Trp Val Arg Arg Val Phe 340 345 350			1056
ctt gac ata gtc cca cgt ctc ctc atg aag cgg ccc tcc aca gtg Leu Asp Ile Val Pro Arg Leu Leu Phe Met Lys Arg Pro Ser Thr Val 355 360 365			1104
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tca cca agg ctt tgg tct gag acc gac atg gag ccc aac ttc act acc Ser Pro Arg Leu Trp Ser Glu Thr Asp Met Glu Pro Asn Phe Thr Thr 385 390 395 400			1200
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ttc tgt gcc cac ctt gag gag cca gcc aaa cct atg tgc aaa tcc cct Phe Cys Ala His Leu Glu Glu Pro Ala Lys Pro Met Cys Lys Ser Pro 420 425 430			1296
tct gga cag tac tca atg ctg cac cct gag ccc cca cag gtg acg tgt Ser Gly Gln Tyr Ser Met Leu His Pro Glu Pro Pro Gln Val Thr Cys 435 440 445			1344
tcc tct ccg aag ccc tcc tgc cac ccc ctg agt gac acc cag acc aca Ser Ser Pro Lys Pro Ser Cys His Pro Leu Ser Asp Thr Gln Thr Thr 450 455 460			1392
tct atc tca aaa ggc aga tcg ctc agt gtt cag cag atg tac agc ccc Ser Ile Ser Lys Gly Arg Ser Leu Ser Val Gln Gln Met Tyr Ser Pro 465 470 475 480			1440
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gcc tct cca gcg tcg cag cgc tgc cac ctc aat gaa gag cag ccc cag Ala Ser Pro Ala Ser Gln Arg Cys His Leu Asn Glu Glu Gln Pro Gln 515 520 525			1584
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LeA34821\_SeqList

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Gly Thr Pro Thr Gln Gly Ser Lys Ser His Ser Asn Lys Gly Glu His	
545 550 555 560	
ctc gtg ctg atg tcc cca gcc ctg aag ctg gcg gtg gaa ggg gtc cac	1728
Leu Val Leu Met Ser Pro Ala Leu Lys Leu Ala Val Glu Gly Val His	
565 570 575	
tac att gca gac cac ctg cga gca gaa gat gca gat ttc tca gtg aag	1776
Tyr Ile Ala Asp His Leu Arg Ala Glu Asp Ala Asp Phe Ser Val Lys	
580 585 590	
gaa gac tgg aag tac gta gca atg gtc att gac cggtt ctc tgg	1824
Glu Asp Trp Lys Tyr Val Ala Met Val Ile Asp Arg Ile Phe Leu Trp	
595 600 605	
atg ttc atc atc gtgttgt ctgggg acc gtt ggg ctc ttc ctc ccg	1872
Met Phe Ile Ile Val Cys Leu Leu Gly Thr Val Gly Leu Phe Leu Pro	
610 615 620	
ccg tgg ctg gca gga atg atc taa	1896
Pro Trp Leu Ala Gly Met Ile	
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<210> 7  
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<212> PRT

<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Modified alpha  
 4 subunit of the chicken nicotinic acetylcholine  
 receptor

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50 55 60	
Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr	
65 70 75 80	
Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp	
85 90 95	
Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu	
100 105 110	
Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe	
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Ala Val Thr His Leu Thr Lys Ala His Leu Phe Tyr Asp Gly Arg Ile  
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 145 150 155 160  
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 165 170 175  
 Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His  
 180 185 190  
 Arg Gly Thr Asn Val Val Glu Leu Gly Val Asp Gln Leu Asp Tyr Trp  
 195 200 205  
 Glu Ser Gly Glu Trp Val Ile Ile Asn Ala Val Gly Asn Tyr Asn Ser  
 210 215 220  
 Lys Lys Tyr Glu Cys Cys Thr Glu Ile Tyr Pro Asp Ile Thr Tyr Ser  
 225 230 235 240  
 Phe Ile Ile Arg Arg Leu Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile  
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 Pro Cys Leu Leu Ile Ser Cys Leu Thr Val Leu Val Phe Tyr Leu Pro  
 260 265 270  
 Ser Glu Cys Gly Glu Lys Ile Thr Leu Cys Ile Ser Val Leu Leu Ser  
 275 280 285  
 Leu Thr Val Phe Leu Leu Leu Ile Thr Glu Ile Ile Pro Ser Thr Ser  
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 305 310 315 320  
 Val Thr Leu Ser Ile Ile Ile Thr Val Phe Val Leu Asn Val His His  
 325 330 335  
 Arg Ser Pro Arg Thr His Thr Met Pro Asp Trp Val Arg Arg Val Phe  
 340 345 350  
 Leu Asp Ile Val Pro Arg Leu Leu Phe Met Lys Arg Pro Ser Thr Val  
 355 360 365  
 Lys Asp Asn Cys Lys Lys Leu Ile Glu Ser Met His Lys Leu Thr Asn  
 370 375 380  
 Ser Pro Arg Leu Trp Ser Glu Thr Asp Met Glu Pro Asn Phe Thr Thr  
 385 390 395 400  
 Ser Ser Ser Pro Ser Pro Gln Ser Asn Glu Pro Ser Pro Thr Ser Ser  
 405 410 415  
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 420 425 430  
 Ser Gly Gln Tyr Ser Met Leu His Pro Glu Pro Pro Gln Val Thr Cys  
 435 440 445  
 Ser Ser Pro Lys Pro Ser Cys His Pro Leu Ser Asp Thr Gln Thr Thr  
 450 455 460

LeA34821\_SeqList

Ser Ile Ser Lys Gly Arg Ser Leu Ser Val Gln Gln Met Tyr Ser Pro  
465 470 475 480  
Asn Lys Thr Glu Glu Gly Ser Ile Arg Cys Arg Ser Arg Ser Ile Gln  
485 490 495  
Tyr Cys Tyr Leu Gln Glu Asp Ser Ser Gln Thr Asn Gly His Ser Ser  
500 505 510  
Ala Ser Pro Ala Ser Gln Arg Cys His Leu Asn Glu Glu Gln Pro Gln  
515 520 525  
His Lys Pro His Gln Cys Lys Cys Lys Cys Arg Lys Gly Glu Ala Ala  
530 535 540  
Gly Thr Pro Thr Gln Gly Ser Lys Ser His Ser Asn Lys Gly Glu His  
545 550 555 560  
Leu Val Leu Met Ser Pro Ala Leu Lys Leu Ala Val Glu Gly Val His  
565 570 575  
Tyr Ile Ala Asp His Leu Arg Ala Glu Asp Ala Asp Phe Ser Val Lys  
580 585 590  
Glu Asp Trp Lys Tyr Val Ala Met Val Ile Asp Arg Ile Phe Leu Trp  
595 600 605  
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<211> 81

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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<210> 9

<211> 81

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 9

ccagtagtcc agttggtcca cacccagttc taccacgttg gttcctctag cctcatcgat 60  
gtgtctcaag tctatcttag c 81

<210> 10

<211> 1869

## LeA34821\_SeqList

<212> DNA  
<213> Artificial Sequence

<220>  
<221> CDS  
<222> (1)..(1866)  
<223> Description of Artificial Sequence: Modified alpha 4 subunit of the chicken nicotinic acetylcholine receptor

<400> 10	48
atg gga ttt ctc gtg tcg aag gga aac ctc ctc ctc ctg ctg tgt gcc	
Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Cys Ala	
1 5 10 15	
agc atc ttc ccc gct ttc ggc cac gtg gaa acg cga gcc cat gcg gag	96
Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu	
20 25 30	
gag cgc ctc ctg aag aaa ctc ttc tcc ggg tat aac aag tgg tcc cgt	144
Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg	
35 40 45	
ccc gtc gcc aac att tcg gat gtg gtc ctg gtc cgc ttc ggc ttg tcc	192
Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser	
50 55 60	
ata gcc cag ctc atc gat gtt gat gag aag aac caa atg atg acc aca	240
Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr	
65 70 75 80	
aat gtg tgg gtg aag cag gag tgg cac gac tac aag ctg cgc tgg gac	288
Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp	
85 90 95	
ccc cag gag tat gaa aac gtc aca tcc atc cga atc ccc tca gag ctc	336
Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu	
100 105 110	
atc tgg agg ccg gac att gtc cta tac aac aat gct gat ggt gac ttt	384
Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe	
115 120 125	
gca gtc acc cac ctg acc aaa gcc cac ctc ttc tat gat ggg aga att	432
Ala Val Thr His Leu Thr Lys Ala His Leu Phe Tyr Asp Gly Arg Ile	
130 135 140	
aaa tgg atg cca cct gcc atc tac aaa agc tcc tgc agc atc gat gtt	480
Lys Trp Met Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser Ile Asp Val	
145 150 155 160	
acc ttc ttc ccc ttt gat cag caa aac tgt aaa atg aaa ttt ggc tct	528
Thr Phe Phe Pro Phe Asp Gln Gln Asn Cys Lys Met Lys Phe Gly Ser	
165 170 175	
tgg aca tat gac aaa gct aag ata gac ttg gtg agc atg cat agc cat	576
Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His	
180 185 190	
gtc gac ctg tcc gag ttc tac acc tcc gtg gag tgg gac atc ctg gag	624
Val Asp Leu Ser Glu Phe Tyr Thr Ser Val Glu Trp Asp Ile Leu Glu	
195 200 205	

## LeA34821\_SeqList

gtg cca gcc gtc agg aac gag aag ttc tac acg tgc tgc gac gag ccc Val Pro Ala Val Arg Asn Glu Lys Phe Tyr Thr Cys Cys Asp Glu Pro 210 215 220	672
tac ctg gac ata acg ttt aac ttc att atc cgg agg ctg ccg ctg ttc Tyr Leu Asp Ile Thr Phe Asn Phe Ile Ile Arg Arg Leu Pro Leu Phe 225 230 235 240	720
tac aca atc aat ttg atc att ccc tgc ctg ctt atc tcc tgc ttg act Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile Ser Cys Leu Thr 245 250 255	768
gtc ctg gtc ttc tac cta ccc tct gag tgc gga gag aag ata acc ttg Val Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly Glu Lys Ile Thr Leu 260 265 270	816
tgc atc tct gtg ctg cta tcc ctc acg gtg ttc ctg ctg ctc atc aca Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu Leu Ile Thr 275 280 285	864
gag atc atc cct tct acc tcc ctg gtc atc ccc ctg ata gga gag tat Glu Ile Ile Pro Ser Thr Ser Leu Val Ile Pro Leu Ile Gly Glu Tyr 290 295 300	912
ctg ctc ttc acc atg ata ttt gtc acc ttg tct atc atc atc act gtc Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Ile Ile Thr Val 305 310 315 320	960
ttt gtg ctc aac gta cac cac cgt tca cca cgt acc cac acg atg cct Phe Val Leu Asn Val His His Arg Ser Pro Arg Thr His Thr Met Pro 325 330 335	1008
gac tgg gtg agg agg gtc ttc ctt gac ata gtc cca cgt ctc ctc ttc Asp Trp Val Arg Arg Val Phe Leu Asp Ile Val Pro Arg Leu Leu Phe 340 345 350	1056
atg aag cgg ccc tcc aca gtg aaa gac aat tgc aag aag ctt att gaa Met Lys Arg Pro Ser Thr Val Lys Asp Asn Cys Lys Lys Leu Ile Glu 355 360 365	1104
tct atg cac aaa cta acc aac tca cca agg ctt tgg tct gag acc gac Ser Met His Lys Leu Thr Asn Ser Pro Arg Leu Trp Ser Glu Thr Asp 370 375 380	1152
atg gag ccc aac ttc act acc tca tcc tcc ccc agc ccc cag agt aat Met Glu Pro Asn Phe Thr Thr Ser Ser Ser Pro Ser Pro Gln Ser Asn 385 390 395 400	1200
gaa cct tca ccc aca tct tcc ttc tgt gcc cac ctt gag gag cca gcc Glu Pro Ser Pro Thr Ser Ser Phe Cys Ala His Leu Glu Glu Pro Ala 405 410 415	1248
aaa cct atg tgc aaa tcc cct tct gga cag tac tca atg ctg cac cct Lys Pro Met Cys Lys Ser Pro Ser Gly Gln Tyr Ser Met Leu His Pro 420 425 430	1296
gag ccc cca cag gtg acg tgt tcc tct ccg aag ccc tcc tgc cac ccc Glu Pro Pro Gln Val Thr Cys Ser Ser Pro Lys Pro Ser Cys His Pro 435 440 445	1344
ctg agt gac acc cag acc aca tct atc tca aaa ggc aga tcg ctc agt Leu Ser Asp Thr Gln Thr Ser Ile Ser Lys Gly Arg Ser Leu Ser 450 455 460	1392

LeA34821\_SeqList

gtt cag cag atg tac agc ccc aat aag aca gag gaa ggg agc atc cgc Val Gln Gln Met Tyr Ser Pro Asn Lys Thr Glu Glu Gly Ser Ile Arg 465 470 475 480	1440
tgt agg tcc cga agc atc cag tac tgt tac ctg cag gag gac tct tcc cys Arg Ser Arg Ser Ile Gln Tyr Cys Tyr Leu Gln Glu Asp Ser Ser 485 490 495	1488
cag acc aat ggc cac tct agt gcc tct cca gcg tcg cag cgc tgc cac Gln Thr Asn Gly His Ser Ser Ala Ser Pro Ala Ser Gln Arg Cys His 500 505 510	1536
ctc aat gaa gag cag ccc cag cac aag ccc cac cag tgc aag tgt aag Leu Asn Glu Glu Gln Pro Gln His Lys Pro His Gln Cys Lys Cys Lys 515 520 525	1584
tgc aga aag gga gag gca gct ggc aca ccg act caa gga agc aag agc Cys Arg Lys Gly Glu Ala Ala Gly Thr Pro Thr Gln Gly Ser Lys Ser 530 535 540	1632
cac agc aac aaa gga gaa cac ctc gtg ctg atg tcc cca gcc ctg aag His Ser Asn Lys Gly Glu His Leu Val Leu Met Ser Pro Ala Leu Lys 545 550 555 560	1680
ctg gcg gtg gaa ggg gtc cac tac att gca gac cac ctg cga gca gaa Leu Ala Val Glu Gly Val His Tyr Ile Ala Asp His Leu Arg Ala Glu 565 570 575	1728
gat gca gat ttc tca gtg aag gaa gac tgg aag tac gta gca atg gtc Asp Ala Asp Phe Ser Val Lys Glu Asp Trp Lys Tyr Val Ala Met Val 580 585 590	1776
att gac cgg atc ttt ctc tgg atg ttc atc atc gtg tgt ttg ctg ggg Ile Asp Arg Ile Phe Leu Trp Met Phe Ile Ile Val Cys Leu Leu Gly 595 600 605	1824
acc gtt ggg ctc ttc ctc ccg ccg tgg ctg gca gga atg atc taa Thr Val Gly Leu Phe Leu Pro Pro Trp Leu Ala Gly Met Ile 610 615 620	1869

<210> 11  
<211> 622  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Modified alpha  
4 subunit of the chicken nicotinic acetylcholine  
receptor

<400> 11  
Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Cys Ala  
1 5 10 15  
Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu  
20 25 30  
Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg  
35 40 45  
Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser

## LeA34821\_SeqList

50	55	60
Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr		
65	70	75
Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp		
85	90	95
Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu		
100	105	110
Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe		
115	120	125
Ala Val Thr His Leu Thr Lys Ala His Leu Phe Tyr Asp Gly Arg Ile		
130	135	140
Lys Trp Met Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser Ile Asp Val		
145	150	155
Thr Phe Phe Pro Phe Asp Gln Gln Asn Cys Lys Met Lys Phe Gly Ser		
165	170	175
Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His		
180	185	190
Val Asp Leu Ser Glu Phe Tyr Thr Ser Val Glu Trp Asp Ile Leu Glu		
195	200	205
Val Pro Ala Val Arg Asn Glu Lys Phe Tyr Thr Cys Cys Asp Glu Pro		
210	215	220
Tyr Leu Asp Ile Thr Phe Asn Phe Ile Arg Arg Leu Pro Leu Phe		
225	230	235
Tyr Thr Ile Asn Leu Ile Pro Cys Leu Leu Ile Ser Cys Leu Thr		
245	250	255
Val Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly Glu Lys Ile Thr Leu		
260	265	270
Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu Ile Thr		
275	280	285
Glu Ile Ile Pro Ser Thr Ser Leu Val Ile Pro Leu Ile Gly Glu Tyr		
290	295	300
Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Ile Ile Thr Val		
305	310	315
Phe Val Leu Asn Val His His Arg Ser Pro Arg Thr His Thr Met Pro		
325	330	335
Asp Trp Val Arg Arg Val Phe Leu Asp Ile Val Pro Arg Leu Leu Phe		
340	345	350
Met Lys Arg Pro Ser Thr Val Lys Asp Asn Cys Lys Lys Leu Ile Glu		
355	360	365
Ser Met His Lys Leu Thr Asn Ser Pro Arg Leu Trp Ser Glu Thr Asp		
370	375	380
Met Glu Pro Asn Phe Thr Thr Ser Ser Pro Ser Pro Gln Ser Asn		

## LeA34821\_SeqList

385	390	395	400
Glu Pro Ser Pro Thr Ser Ser Phe Cys Ala His Leu Glu Glu Pro Ala			
405	410	415	
Lys Pro Met Cys Lys Ser Pro Ser Gly Gln Tyr Ser Met Leu His Pro			
420	425	430	
Glu Pro Pro Gln Val Thr Cys Ser Ser Pro Lys Pro Ser Cys His Pro			
435	440	445	
Leu Ser Asp Thr Gln Thr Thr Ser Ile Ser Lys Gly Arg Ser Leu Ser			
450	455	460	
Val Gln Gln Met Tyr Ser Pro Asn Lys Thr Glu Glu Gly Ser Ile Arg			
465	470	475	480
Cys Arg Ser Arg Ser Ile Gln Tyr Cys Tyr Leu Gln Glu Asp Ser Ser			
485	490	495	
Gln Thr Asn Gly His Ser Ser Ala Ser Pro Ala Ser Gln Arg Cys His			
500	505	510	
Leu Asn Glu Glu Gln Pro Gln His Lys Pro His Gln Cys Lys Cys Lys			
515	520	525	
Cys Arg Lys Gly Glu Ala Ala Gly Thr Pro Thr Gln Gly Ser Lys Ser			
530	535	540	
His Ser Asn Lys Gly Glu His Leu Val Leu Met Ser Pro Ala Leu Lys			
545	550	555	560
Leu Ala Val Glu Gly Val His Tyr Ile Ala Asp His Leu Arg Ala Glu			
565	570	575	
Asp Ala Asp Phe Ser Val Lys Glu Asp Trp Lys Tyr Val Ala Met Val			
580	585	590	
Ile Asp Arg Ile Phe Leu Trp Met Phe Ile Ile Val Cys Leu Leu Gly			
595	600	605	
Thr Val Gly Leu Phe Leu Pro Pro Trp Leu Ala Gly Met Ile			
610	615	620	

&lt;210&gt; 12

&lt;211&gt; 79

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer<400> 12  
caacagcaag aaatatgaat gctgcgacga gccctacctt gatataactt tcaacttcat 60  
tatccggagg ctgccgctg 79

&lt;210&gt; 13

&lt;211&gt; 79

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 13  
cagcggcagc ctccggataa tgaagttgaa agttatatca agtagggct cgtcgagca 60  
ttcatatttc ttgctgttg 79

<210> 14  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 14  
gaacaaaagc tggaggtcca ccgcggtggc 30

<210> 15  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 15  
gccaccgcgg tggacctcca gctttgttc 30

<210> 16  
<211> 75  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 16  
gcggggagtg ggtcatctta gaagtccgg ccgttcgcaa cgaaaagttt tatacatgct 60  
gcgacgagcc ctacc 75

<210> 17  
<211> 75  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 17  
ggtagggctc gtcgcagcat gtataaaact tttcggtcg aacggccggg acttcaatga 60  
tgacccactc cccgc